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Population and host plant differentiation of the sweetpotato whitefly, *Bemisia tabaci* (Homoptera: Aleyrodidae), in East, South and Southwest China

Muhammad Z. AHMED[1], SHEN Yuan[2], JIN Gui-Hua[1], REN Shun-Xiang[1], DU Yu-Zhou[2], QIU Bao-Li [1,*]

(1. Department of Entomology, South China Agricultural University, Guangzhou 510640, China;
2. Department of Plant Protection, Yangzhou University, Yangzhou, Jiangsu 225009, China)

Abstract: The sweetpotato whitefly, *Bemisia tabaci* (Gennadius), is a species complex that is considered an important agricultural pest because of its diversity in biotypes, capacity to transmit viruses, high resistance to chemicals and rapid physiological development. Its biotype status in Jiangsu, Guangdong and Yunnan provinces was determined by using mitochondrial DNA COI markers and correlated with their host plants and locations. Results indicated that, in Guangdong and Yunnan, the local unresolved biotypes and the already known biotypes of *B. tabaci* (B and Q) coexist, the former is relatively more dependent on its host plants than the invasive biotypes. No Q biotype of *B. tabaci* has been found in Guangdong and no local biotype has been found in Jiangsu in this study. Multitudinous host plants and the inherent polyphagous characteristics enhance the wide invasion of B and Q biotypes in different counties.

Key words: *Bemisia tabaci*; biotype; host plant; geographical location; China

1 INTRODUCTION

The sweetpotato whitefly *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae), also known as the cotton or tobacco whitefly, has become one of the most devastating tropical and sub-tropical worldwide agricultural pests (Byrne and Bellows, 1991) in the past 20 years (Anthony *et al.*, 1995; De Barro, 1995; Perring, 2001). This cosmopolitan pest affects the yield of a broad range of agricultural, fiber, vegetable and ornamental crops (Cahill *et al.*, 1996) by causing damage through feeding directly on the plant sap, and indirectly through excretion of honeydews that produces sooty mould. These sooty mold fungi, using honeydew as a substrate, colonize contaminated surfaces, further interfering with photosynthesis and ultimately resulting in reduced quality of fruit and fiber (Byrne and Bellows, 1991). In addition, *B. tabaci* is the vector of several economically important plant viral-pathogens, these could be more than 110 plant viruses, most of them belong to begomovirus (Geminiviridae), which has been recognized as the most important emerging plant virus group in sub-tropical and tropical world regions (Brown, 1990, 2000; Martin *et al.*, 2000; Jones, 2003; Mughra *et al.*, 2008). *B. tabaci* is a genetically diverse group (Frohlich *et al.*, 1999; De Barro *et al.*, 2000) and its genetic complexity was first recognized in the 1950s when morphologically indistinguishable populations were reported to differ in host range, host plant adaptability, and plant virus-transmission capabilities (Bird, 1957; Mound, 1963; Costa and Russell, 1975; Bird and Maramorosch, 1978). This led to the development of the concept that *B. tabaci* was composed of a series of biotypes (Costa and Brown, 1991; Bedford *et al.*, 1994). Since then, there has been a proliferation of biotypes described with the current count exceeding 20 (Perring, 2001) and more recently, its global populations known have been grouped into 12 genetically distinct groups (Boykin *et al.*, 2007). The considerable genetic diversity of *B. tabaci*, while retaining identical morphological characters, with various complexity of their biological interactions and their varying abilities to interbreed, have led to the belief that *B. tabaci* represents a cryptic species complex (Bedford *et al.*, 1994; Brown *et al.*, 1995; Byrne *et al.*, 1995; Moya *et al.*, 2001;

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First author: Muhammad Zaheerudin Ahmed, born in 1983, male, works on insect molecular ecology, now a common wealth scholar for PhD at University of Pretoria, South Afica, E-mail: zaheerento@gmail.com

* Author for correspondence, E-mail: baileyqiu@yahoo.com.cn

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Pascual and Callejas, 2004; De Barro *et al*., 2006; Qiu *et al*., 2007).

B. tabaci outbreaks caused by native and introduced variants are often not immediately recognized until populations have reached uncontrollable levels. Although not all populations have the same propensity to achieve pest or vector status and not all of them are capable of long-distance spread, the B and Q biotypes are exceptions known to be invasive and have spread worldwide (Frohlich *et al*., 1999; De Barro *et al*., 2000, 2005; De Barro, 2005; Martinez-Carrillo and Brown 2007; Qiu *et al*., 2007). Furthermore, in *B. tabaci* biotypes, B and Q are polyphagous, and other biotypes might differ from them in host plant specialization. It has already been reported that the *B. tabaci* species complex has over 600 host plants, including numerous economically significant horticultural and ornamental species (Mound and Halsey, 1978; Secker *et al*., 1998). The reasons behind, the worldwide spread of B and Q biotypes are complicated, but it has been thought that, it could be associated with the international trades of ornamental and other economically important crops (Brown *et al*., 1995; Perring, 2001; Reitz, 2007).

In China, *B. tabaci* was not considered as a serious pest until its outbreak in the mid-1990s, which was due to the invasion of the B biotype (De Barro *et al*., 2005). This biotype has caused serious damage to a wide range of vegetables, fiber crops, and ornamental plants in more than 30 provinces in China (Qiu *et al*., 2007, 2008). Moreover, the Q biotype, which was recorded in 2004 in Yunnan Province, Southwest China in 2003 (Chu *et al*., 2005), has also been found on various host plants in Beijing (Zhang *et al*., 2005), Jiangsu (Shen, 2007), and Zhejiang provinces (Xu *et al*., 2006). In addition to the invasive biotypes, some native populations or haplotypes of *B. tabaci*, such as the Cv and ZhJ-2 populations, also cause serious damage to their specific host plants (Qiu *et al*., 2006; Zang and Liu, 2007). Preliminary field investigation indicated that most of the native *B. tabaci* populations are oligophagous.

It has always been problematic to identify these various biotypes of *B. tabaci* morphologically, however, molecular sequence analysis of the mitochondrial cytochrome oxidase I gene (mtCOI) has been recognized as one of the most useful molecular markers for differentiating *B. tabaci* populations and for identifying these genetically diverse populations (Bird and Maramorosch, 1978; Costa and Brown, 1991; Brown *et al*., 1995; Guirao *et al*., 1997; Frohlich *et al*., 1999; Berry *et al*., 2004; Brown, 2000; Qiu *et al*., 2007). Population differentiation plays an important role in revealing an organism's evolutionary history, including the *B. tabaci* species complex, but this has not been clearly reported in China. In this study, the biotype/haplotype and host plants of *B. tabaci* populations in eastern, southern and southwestern parts of China are investigated by sequencing the mitochondrial COI gene of various *B. tabaci* populations, collected from multiple plant hosts throughout China; the results may show us the relationships between population differentiation, host plants and geographical distribution of the *B. tabaci* samples, which will help us to estimate the spread of different *B. tabaci* populations in the future.

2 MATERIALS AND METHODS

2.1 Insects

Whitefly adults were collected from the fields using a hand-held aspirator and preserved immediately in 95% ethanol for later processing, and their host plants were taken back to the laboratory for species identification simultaneously. A total of 167 samples, each approximately 100 - 500 individuals, were collected from 11 different provinces during 2006 - 2008. *B. tabaci* populations collected from Jiangsu, Guangdong and Yunnan provinces were investigated as representatives in this study due to the rich biodiversities of both *B. tabaci* populations and their host plants, all the *B. tabaci* samples from these provinces are abundant (350 - 450 adults) in population and their host plants are from various species. Their locations and host plants were showed in Table 1.

2.2 Biotype identification of the *B. tabaci* samples

2.2.1 DNA extraction: DNA was extracted from individual insect of each sample. The *B. tabaci* samples were firstly washed using double distilled water to remove alcohol, then they were homogenized individually in 200 μL lysis buffer (1% SDS, 10 mmol/L Tris-HCl, pH 8.0, 25 mmol/L EDTA, 25 mmol/L NaCl, 1.0 mg/mL proteinase K) for 30 s, in a 1.5 mL microcentrifuge tube. The homogenate was incubated at 55℃ for 2 - 3 h, after which the homogenate was centrifuged for 5 min at 5 000 rpm and the suspension was moved to a new 1.5 mL microcentrifuge tube and used for PCR amplification directly or stored at -20℃ for further use.

2.2.2 PCR amplification: The mitochondrial COI gene was used to identify the biotype of the representative samples of *B. tabaci*. Primers used to amplify the mtCOI gene fragment were C1-J-2195 (5′ TTGATTTTTTGGTCATCCAGAAGT-3′) and L2-N-3014 (5′-TCCAATGCACTAATCTGCCATATTA-3′). PCR reactions (25 μL) contained 2.0 μL of each template DNA, 2 μmol/L $MgCl_2$, 25 pmol/L for each primer, 2.5 mmol/L of each dNTP, 1.0 μL Express Taq polymerase (5 U/ μL, TaKaRa) and 1 × PCR buffer. PCR amplifications were done in a Bio-Rad thermocycler and included a precycle denaturation step for 2 min at 94℃; followed by 35 cycles at 95℃ for 1 min, 50℃ for 1 min, and 72℃ for 1 min; and a final extension at 72℃ for 10 min. The PCR products were electrophoresised on 0.8% agarose gels, and bands were visualized using ethidium bromide staining under an ultraviolet light. Those products that yielded a band with the expected size of 820 – 850 bp were sequenced on an ABI377 automated DNA Sequencer (PE Applied Biosystems). At least 5 individuals of each *B. tabaci* samples were repeated for PCR application and COI sequencing.

Table 1 Samples collected from different locations and host plants in China

Codes	Collection sites	Biotype	Host plant	Host plant family	GenBank accession no. of mt COI	Locations
Ast-GGD	Zhaoqing, Guangdong	Non-B/Q	*Lactuca sativa* (lettuce)	Asteraceae	EU192034	23° 02′ 53″ N, 112° 27′ 54″ E
Con-GGD1	Yingde, Guangdong	Non-B/Q	*Ipomoea batatas* (sweet potato)	Convolvulaceae	EU192036	24° 00′ 09″ N, 113° 27′ 20″ E
Con-GGD2	Zhanjiang, Guangdong	Non-B/Q	*Ipomoea batatas* (sweet potato)	Convolvulaceae	EU192037	21° 16′ 14″ N, 110° 21′ 33″ E
Con-GGD3	Yangjiang, Guangdong	Non-B/Q	*Ipomoea batatas* (sweet potato)	Convolvulaceae	EU192038	21° 51′ 27″ N, 111° 58′ 57″ E
Con-GGD4	Shaoguan, Guangdong	Non-B/Q	*Ipomoea batatas* (sweet potato)	Convolvulaceae	EU192040	24° 48′ 39″ N, 113° 35′ 60″ E
Con-GGD5	Guangzhou, Guangdong	Non-B/Q	*Ipomoea batatas* (sweet potato)	Convolvulaceae	EU192042	23° 07′ 44″N, 113° 15′ 51″ E
Eup-GGD	Shenzhen, Guangdong	Non-B/Q	*Codiaeum variegatum* (croton)	Euphorbiaceae	EU192043	22° 32′ 36″N, 114° 03′ 28″ E
Leg-GGD	Meizhou, Guangdong	Non-B/Q	*Vicia faba* (horsebean)	Leguminosae	EU192039	24° 17′ 18″ N, 116° 07′ 20″ E
Sol-YUN1	Baoshan, Yunnan	Non-B/Q	*Lycopersicon esculentum* (tomato)	Solanaceae	EU192052	25° 06′ 43″ N, 99° 09′ 41″ E
Sol-YUN2	Mengla, Yunnan	Non-B/Q	*Lycopersicon esculentum* (tomato)	Solanaceae	EU192054	21° 28′ 00″ N, 101° 35′ 00″ E
Sol-YUN3	Yuanjiang, Yunnan	Non-B/Q	*Solanum melongena* (eggplant)	Solanaceae	EU192060	23° 48′ 20″ N, 102° 05′ 35″ E
Sol-YUN4	Jinghong, Yunnan	Q	*Lycopersicon esculentum* (tomato)	Solanaceae	EU192061	22° 00′ 45″ N, 100° 47′ 36″ E
Sol-YUN5	Yuanjiang, Yunnan	Non-B/Q	*Solanum melongena* (eggplant)	Solanaceae	EU192060	23° 48′ 20″ N, 102° 05′ 35″ E
Sol-YUN6	lincang, Yunnan	Non-B/Q	*Lycopersicon esculentum* (tomato)	Solanaceae	EU192056	22° 31′ 60″ N, 99° 55′ 60″ E
Con-YUN1	Jinghong, Yunnan	Non-B/Q	*Ipomoea batatas* (sweet potato)	Convolvulaceae	EU192053	22° 00′ 45″ N, 100° 47′ 36″ E
Con-YUN2	Ruili, Yunnan	B	*Ipomoea batatas* (sweet potato)	Convolvulaceae	EU192055	24° 00′ 589″ N, 97° 51′ 11″ E
Con-YUN4	Menghai, Yunnan	Non-B/Q	*Ipomoea batatas* (sweet potato)	Convolvulaceae	EU192058	21° 58′ 58″ N, 100° 25′ 43″E
Con-YUN5	Pingbian, Yunnan	Non-B/Q	*Ipomoea batatas* (sweet potato)	Convolvulaceae	EU192059	22° 59′ 06″ N, 103° 41′ 10″ E
Eup-YUN	Kunming, Yunnan	Q	*Euphorbia pulcherrima* (poinsettia)	Euphorbiaceae	EU192049	25° 02′ 20″ N, 102° 43′ 19″ E
Sol-JSU1	Dongtai, Jiangsu	B	*Solanum melongena* (eggplant)	Solanaceae	EU192070	35° 50′ 45″ N, 120° 18′ 05″ E
Sol-JSU2	Suqian, Jiangsu	Q	*Solanum melongena* (eggplant)	Solanaceae	EU192071	33° 56′ 57″ N, 118° 17′ 45″ E
Sol-JSU3	Nantong, Jiangsu	B	*Solanum melongena* (eggplant)	Solanaceae	EU263628	32° 10′ 14″ N, 121° 04′ 28″ E
Sol-JSU4	Haimen, Jiangsu	Q	*Lycopersicon esculentum* (tomato)	Solanaceae	EU263629	31° 53′ 32″ N, 121° 09′ 12″ E
Con-JSU1	Changshu, Jiangsu	Q	*Lablab purpureus* (hyacinth-bean)	Convolvulaceae	EU192072	31° 38′ 39″ N, 120° 44′ 17″ E
Con-JSU2	Dafeng Jiangsu	Q	*lpomoea purpurea* (sweet potato)	Convolvulaceae	EU263630	33° 12′ 00″ N, 120° 28′ 00″ E
Cru-JSU	Dafeng, Jiangsu	B	*Brassica napus* (rape)	Cruciferae	EU263625	33° 12′ 00″ N, 120° 28′ 00″ E
Cuc-JSU	Dafeng, Jiangsu	Q	*Cucumis sativus* (cucumber)	Cucurbitaceae	EU263633	33° 12′ 00″ N, 120° 28′ 00″ E
Mal-JSU	Xinghua, Jiangsu	B	*Gossypium herbaceum* (cotton)	Malvaceae	EU263627	32° 36′ 25″ N, 119° 00′ 25″ E
Vit-JSU	Dafeng, Jiangsu	Q	*Parthenocissus tricuspidata* (Boston ivy)	Vitaceae	EU263631	33° 12′ 00″ N, 120° 28′ 00″ E

2.3 Data analysis

For the 5 repeated COI sequences of each *B. tabaci* population, they were firstly analyzed and aligned with DNAStar (Lasergene5.0), and the most accurate sequence was selected to represent this population. Then, the representative sequences from different *B. tabaci* populations were compared using ClustalX1.83. The genetic distances between different biotypes of *B. tabaci* were calculated based on their COI sequences, and their phylogenetic relationships were calculated using ME (Minimum Evolution) method in MEGA v. 3. 1 (Bootstrap = 1 000). Some COI sequences of *B. tabaci* populations from Spain, Morocco and USA as well as from China were downloaded from GenBank and used as reference sequences. The A biotype from USA (DQ174542) and the greenhouse whitefly Trialeurodes vaporariorum, (AF418672) were used as a species and genus outgroup in the phylogenetic tree (Table 2).

Table 2 Samples downloaded from GenBank and used as reference in phylogenetic tree

Code/biotype	Location	Host plant	Host plant family	GenBank accession no. of mt CO1
Morocco/Q	Nador, Morocco	N/A	N/A	AJ517769
Spain/Q	Spain	N/A	N/A	EU427719
Eup-USA /B	Florida, USA	*Euphorbia pulcherrima* (poinsettia)	Euphorbiaceae	EU427727
Fab-GGD/B	Guangzhou, China	*Glycine max* (soybean)	Fabaceae	EU192032
Con-Zhj-2-1	Zhejiang, China	*lpomoea purpurea* (sweet potato)	Convolvulaceae	DQ309077
Con-Zhj-2-2	Zhejiang, China	*lpomoea purpurea* (sweet potato)	Convolvulaceae	AJ867557
USA/A	USA	N/A	N/A	DQ174542
Trialeurodes vaporariorum	Bangalore, India	*Phyllanthus emblica* (Amla)	Phyllanthaceae	AF418672

N/A: not available.

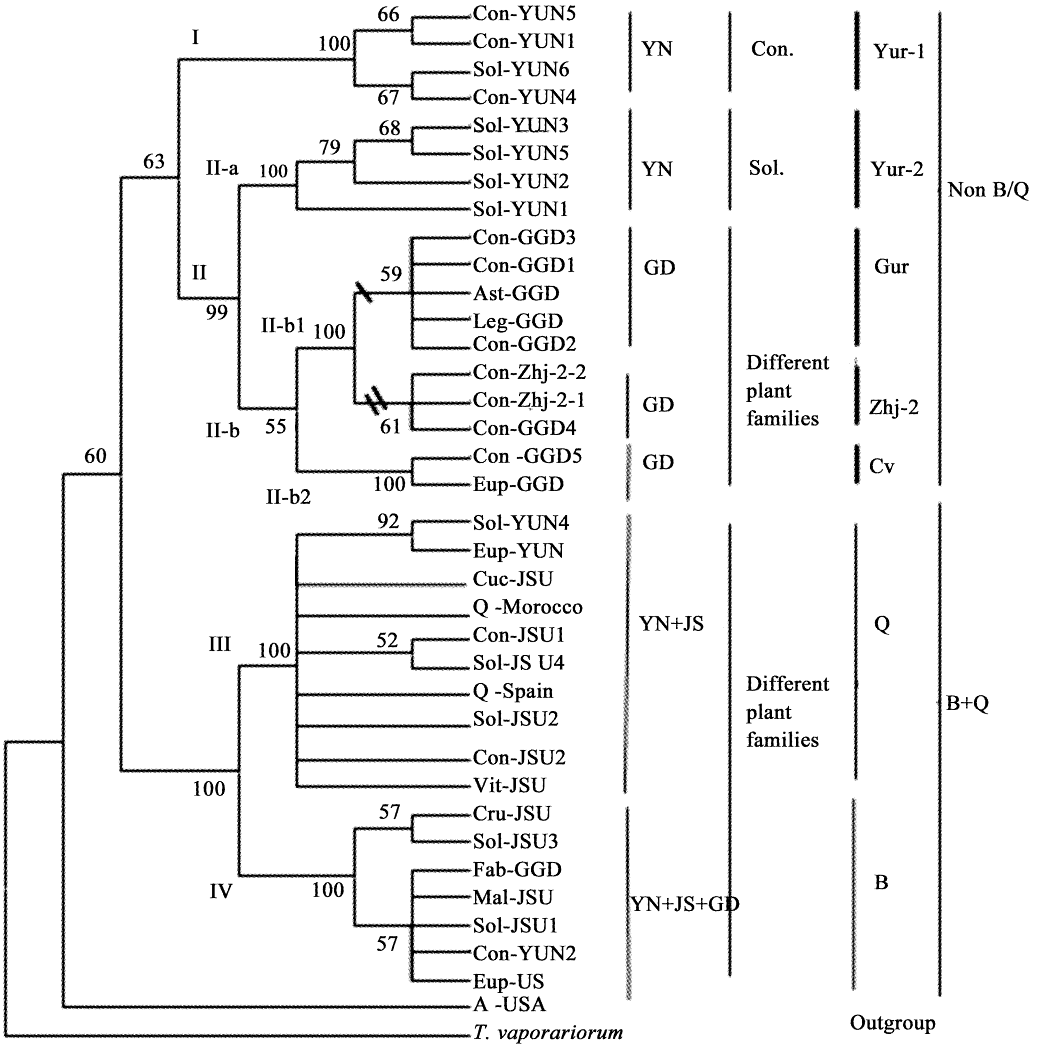

Fig. 1 Strict consensus phylogenetic tree of *Bemisia tabaci* based on CO I sequences
The tree has been constructed by the ME (Minimum Evolution) method in MEGA v. 3. 1 (Bootstrap = 1 000) to show relationships among different *Bemisia tabaci* biotypes. The sequence of the greenhouse whitefly *Trialeurodes vaporariorum* (AF418672 TV) was used as outgroup.

3 RESULTS

3.1 Phylogenetic relationships of different *B. tabaci* populations

The phylogenetic relationship of all the *B. tabaci* populations collected from Guangdong, Jiangsu and Yunnan provinces is shown in Fig. 1. Results revealed that all the Chinese populations are clustered into two groups, the non-B/Q group and the B/Q group. For the non-B/Q group, there are two branches (branch I and II); samples in the first branch are from Yunnan, and all of their host plants belonged to the Convolvulaceae family, the biotype of this branch was named Yur-1 (Yunnan unresolved-1) in this study. Meanwhile, samples in the second branch were divided into two sub-branches, the samples in II-a sub-branch are also from Yunnan, but their host plants belong to the Solanaceae family, the biotype of this sub-branch was named as Yur-2 temporarily in present study. The II-b sub-branch includes several populations from Guangdong; their host plants are more diverse, including Convolvulaceae, Asteraceae, Leguminosae, Euphorbiaceae. The biotype of these samples includes the already known biotypes Zhj-2, Cv as well as one unresolved biotype, which was named Gur (Guangdong unresolved) biotype temporarily in this study, and we also found that the Zhj-2 biotype was more close to the Gur population, than the Cv biotype.

Phylogenetic relationships of the *B. tabaci* populations in the B and Q group are simpler than that of non-B/Q group. All the Q biotype samples from Yunnan, Jiangsu and two reference populations from Morocco and Spain were clustered into the III branch, and all the B biotype samples were clustered into the IV branch. The host plants of the Q and B biotype populations are more varied, including seven plant families, Convolvulaceae, Euphorbiaceae, Solanaceae, Cruciferae, Cucurbitaceae, Malvaceae and Vitaceae.

3.2 Genetic distances between different biotypes of *B. tabaci* Chinese populations

The genetic distances between different biotypes of *B. tabaci* are shown in Table 3. Results indicated that the genetic distances of Cv with Zhj-2 and Gur are 0.0988 and 0.966, respectively, while that between Zhj-2 and Gur is 0.0019, which indicates the closer relationship of Zhj-2 and Gur. However, the genetic distances between different branches are waved due to population differentiation. For example, the distance between B and Q is very close (0.0608) while that between Yur-1 and Yur-2 is much larger (0.1662).

Table 3 Genetic distances among different biotypes/ genetic groups of whiteflies based on their CO I sequences

Biotype/genetic groups	B	Q	Cv	Zhj-2	Gur*	Yur-1*	Yur-2*
B	Q	0.0608					
Cv	0.1832	0.1793					
Zhj-2	0.1712	0.1770	0.0988				
Gur	0.1717	0.1765	0.0966	0.0019			
Yur-1	0.1685	0.1746	0.1490	0.1536	0.1717		
Yur-2	0.1832	0.1789	0.1098	0.1145	0.1144	0.1662	

* Biotype/haplotype that is unresolved in Guangdong and Yunnan provinces.

4 DISCUSSION

The first report of *B. tabaci* in China was in 1949 (Chou, 1949), and its biotype diversity has not been considered until the invasion of the exotic B biotype (Qiu *et al*., 2005). In China, especially in Guangdong and Jiangsu, it has been reported that there are at least 200 plant species that can be attacked by *B. tabaci* (Qiu *et al*., 2001; Zhou *et al*., 2004). On the other hand, many local or unresolved biotypes/haplotypes of *B. tabaci* populations have been found recently in different limited locations, and the known diversity of this pest is still increasing. Boykin *et al*. (2007) resolved the world phylogeny of *B. tabaci* species complex into 12 major genetic groups. The two most invasive *B. tabaci*, B and Q biotypes were classified into the Mediterranean/Asia Minor/Africa group and Mediterranean group respectively while other all Non B/Q biotypes as the China are classified in China group by Boykin *et al*. (2007).

The *B. tabaci* samples collected from Guangdong, Jiangsu and Yunnan provinces were analyzed in this study; it has been found that there are B, Q and at least two local unresolved biotypes (Yur-1 and Yur-2) in Yunnan. In Guangdong, there are B, Cv, Zhj-2 and a local unresolved biotype (Gur) while Q biotype was not found in the samples collected from Guangdong. However, in Jiangsu province, only the two invasive biotypes, B and Q were found in this study. *B. tabaci* is considered a globally quarantine species in regards to international trade in a range of plant and plant product commodities, and it also has been suggested to use strict quarantine measurement during trade inside the country to stop the movement of these biotypes (both native and invasive biotypes).

In the case of host plant specialization, it is interesting that all the non-B/Q biotype populations in Yunnan province are divided into two groups; Yur-1 and Yur-2 and their host plants are quite simple; all of Yur-1 belonged to Convolvulaceae while those of Yur-2 belonged to Solanaceae family. However, those of the non-B/Q biotypes from Guangdong province are quite complex (Fig. 1). It may indicate that the non-B/Q biotype populations in Yunnan province are more dependent on their host plants, compared to those *B. tabaci* populations from Guangdong. Geographic barriers alone could not explain all the observed genetic variations while differential host plant utilization explained one of the reasons for genetic variation in non-B/Q samples but could not explain the overall cause for these variations. Furthermore, roles of mating interference and Wolbachia in developing the genetic structure could not be ignored (De Barro, 2005; Ahmed, 2008). Chinese populations of *B. tabaci* used in this study, have already been investigated to be positive for Wolbachia infections (Ahmed, 2008). As far as Q and B biotype *B. tabaci* concerned, they had been collected from various host plants which are divided into seven plant families. This might confirm the hypothesis that a wide range of host plants is one of the reasons that the exotic B and Q biotype populations could settle down easily in new places through avoiding population from dying out (Brown *et al*., 1995). Furthermore, no Q biotype has been found in Guangdong till now, although we do not know if it already exists. Therefore, more monitoring work should be done in the future.

In conclusion, the results of this study suggest that, in eastern, southern and southwestern China, the local unresolved biotypes and the already known biotypes of *B. tabaci* (B and Q) coexist and the non-B/Q biotypes relatively more dependent on their host plants than the invasive biotypes. More work should been done to investigate and control the concurrent damages from both invasive and indigenous biotypes of *B. tabaci* in the future.

References

Ahmed MZ, 2008. Molecular Identification and Phylogeny of *Bemisia tabaci* and Its *Wolbachia*. Msc Thesis, South China Agricultural University, Guangzhou. 92 – 95. [Ahmed MZ, 2008, 烟粉虱及其共生菌 *Wolbachia* 的分子鉴定及其系统发育研究. 广州: 华南农业大学硕士学位论文. 92 – 95]

Anthony NM, Brown JK, Markham PG, Ffrenchconstant RH, 1995. Molecular analysis of cyclodiene resistance-associated mutations among populations of the sweetpotato whitefly *Bemisia tabaci*. *Pest Biochem. Physiol*., 51: 220 – 228.

Bedford ID, Briddon R, Brown JK, Rosell RC, Markham PG, 1994. Geminivirus-transmission and biological characterisation of *Bemisia tabaci* (Gennadius) biotypes from different geographic regions. *Ann. Entomol. Soc. Am*., 125: 311 – 325.

Berry S, Rey MEC, Rogan D, Fondong VN, Fauquet CM, Brown JK, 2004. Molecular evidence for distinct *Bemisia tabaci* geographical genotypes from cassava in Africa. *Ann. Entomol. Soc. Am*., 97: 852 – 859.

Bird J, 1957. A Whitefly Transmitted Mosaic *Jatropha gossypifolia*. Technical Paper, Agricultural Experiment Station, Puerto Rico. 22: 1 – 35.

Bird J, Maramorosch K, 1978. Viruses and virus diseases associated with whiteflies. *Adv. Virus Res*., 71: 233 – 260.

Boykin LM, Shatters Jr RG, Rosell RC, McKenzie CL, Bagnall RA, De Barro P, Frohlich DR, 2007. Global relationships of *Bemisia tabaci* (Hemiptera: Aleyrodidae) revealed using Bayesian analysis of mitochondrial COI DNA sequences. *Mol. Phyl. Evol*., 44: 1 306 – 1 319.

Brown JK, 1990. An update on the whitefly-transmitted geminiviruses in the Americas and the Caribbean Basin. *FAO Plant Prot. Bull*., 39: 5 – 23.

Brown JK, 2000. Molecular markers for the identification and global tracking of whitefly vector-Begomovirus complexes. *Virus Res*., 71: 233 – 260.

Brown JK, Frohlich DR, Rosell RC, 1995. The sweetpotato or silverleaf whiteflies: Biotypes of *Bemisia tabaci* (Genn.), or a species complex? *Ann. Rev. Entomol*., 40: 511 – 534.

Byrne DN, Bellows Jr TS, 1991. Whitefly biology. *Ann. Rev. Entomol*., 36: 431 – 457.

Byrne FJ, Cahill M, Denholm I, Devonshire AL, 1995. Biochemical identification of interbreeding between B-type and non B-type strains of the tobacco whitefly *Bemisia tabaci*. *Biochem. Genet*., 33: 13 – 23.

Cahill M, Denholm I, Ross G, Gorman K, Johnston D, 1996. Relationship between bioassay data and the simulated field performance of insecticides against susceptible and resistant adult *Bemisia tabaci*. *Bull. Entomol. Res*., 86: 109 – 116.

Chou I, 1949. List of whitefly species in China. *J. Chinese Entomol*., 3: 1 – 18.

Chu D, Zhang YJ, Cong B, Xu BY, Wu QJ, 2005. Identification for Yunnan Q-biotype *Bemisia tabaci* population. *Chinese Bull. Entomol*., 42: 54 – 56. [褚栋, 张友军, 丛斌, 徐宝云, 吴青君, 2005. 云南 Q 型烟粉虱种群的鉴定. 昆虫知识, 42: 54 – 56]

Costa AS, Russell LM, 1975. Failure of *Bemisia tabaci* to breed on cassava plants in Brazil (Homoptera: Aleyroidea). *Cienc. Cult*., 27: 390 – 399.

Costa HS, Brown JK, 1991. Variation in biological characteristics and esterase patterns among populations of *Bemisia tabaci*, and the association of one population with silverleaf symptom development. *Entomol. Exp. Appl*., 61: 211 – 219.

De Barro PJ, 1995. *Bemisia tabaci* biotype B: a review of its biology, distribution and control. *CSIRO Division of Entomology Technical Paper*, 36: 58.

De Barro PJ, 2005. Genetic structure of the whitefly *Bemisia tabaci* in the Asia-Pacific region revealed using microsatellite markers. *Mol. Ecol*., 14: 3 695 – 3 718.

De Barro PJ, Bourne A, Khan SA, Brancatini VAL, 2006. Host plant and biotype density interactions (their role in the establishment of the invasive B biotype of *Bemisia tabaci*. *Biol. Invasions*, 8: 287 – 294.

De Barro PJ, Driver F, Trueman JWH, Curran J, 2000. Phylogenetic relationships of world populations of *Bemisia tabaci* (Gennadius) using ribosomal ITS1. *Mol. Phylogenet. Evol*., 16: 29 – 36.

De Barro PJ, Trueman JWH, Frohlich DR, 2005. *Bemisia argentifolii* is a race of *B. tabaci* (Hemiptera: Aleyrodidae): the molecular genetic differentiation of *B. tabaci* populations around the world. *Bull. Entomol. Res*., 95: 193 – 203.

Frohlich DR , Torres-Jerez II, Bedford ID, Markham PG, Brown JK,

1999. A phylogeographical analysis of the *Bemisia tabaci* species complex based on mitochondrial DNA markers. *Mol. Ecol.*, 8: 1 683 - 1 691.

Guirao P, Beitia F, Cenis JL, 1997. Biotype determination of Spanish population of *Bemisia tabaci* (Homoptera: Aleyrodidae). *Bull. Entomol. Res.*, 87: 587 - 593.

Jones DR, 2003. Plant viruses transmitted by whiteflies. *Eur. J. Plant Pathol.*, 109: 195 - 219.

Martin JH, Mifsud D, Rapisarda C, 2000. The whiteflies (Hemiptera: Aleyrodidae) of Europe and the Mediterranean Basin. *Bull. Entomol. Res.*, 90: 407 - 448.

Martinez-Carrillo JL, Brown JK, 2007. First report of the Q biotype of *Bemisia tabaci* in southern Sonora, Mexico. *Phytoparasitica*, 35: 282 - 284.

Mound LA, 1963. Host-correlated variation in *Bemisia tabaci* (Gennadius) (Homoptera: Aleyroideae). *Proc. R. Entomol. Soc. Lond.*, 38: 171 - 180.

Mound LA, Halsey SH, 1978. Whitefly of The World. A Systematic Catalogue of the Aleyrodidae with Host Plant and Natural Enemy Data. British Museum (Natural History) and Chichester. John Wiley & Sons, London, UK. 340 pp.

Moya A, Guirao P, Cifuentes D, Beitia F, Cenis JL, 2001. Genetic diversity of Iberian populations of *Bemisia tabaci* (Hemiptera: Aleyrodidae) based on random amplified polymorphic DNA-polymerase chain reaction. *Mol. Ecol.*, 10: 891 - 897.

Mughra RB, Liu SS, Zhou X, 2008. Tomato yellow leaf curl virus and tomato leaf curl Taiwan virus invade south-east coast of China. *J. Phytopathol.*, 156: 217 - 221.

Pascual S, Callejas C, 2004. Intra- and interspecific competition between biotypes B and Q of *Bemisia tabaci* (Hemiptera: Aleyrodidae) from Spain. *Bull. Entomol. Res.*, 94: 369 - 375.

Perring TM, 2001. The *Bemisia tabaci* species complex. *Crop Protection*, 20: 725.

Qiu BL, Coats SA, Ren SX, Dris AM, Xu CX, Brown JK, 2007. Phylogenetic relationships of native and introduced *Bemisia tabaci* (Homoptera: Aleyrodidae) from China and India based on mtCOI DNA sequencing and host plant comparisons. *Prog. Nat. Sci.*, 17: 645 - 654.

Qiu BL, De Barro PJ, Ren SX, 2005. Development, survivorship and reproduction of *Eretmocerus* sp. nr. *furuhashii* (Hymenoptera: Aphelinidae) parasitizing *Bemisia tabaci* (Hemiptera: Aleyrodidae) on glabrous and non-glabrous host plants. *Bull. Entomol. Res.*, 95: 313 - 319.

Qiu BL, Mandour NS, Xu CX, Ren SX, 2008. Evaluation of the entomopathogenic nematode, *Steinernema feltiae*, as a biological control agent of the whitefly, *Bemisia tabaci*. *Int. J. Pest Manag.*, 54: 247 - 253.

Qiu BL, Ren SX, Sun TX, Lin L, Kuang ZB, 2001. Investigation of host plants of *Bemisia tabaci* (Gennadius) in Guangzhou area. *J. South China Agric. Univ.*, 22: 43 - 47. [邱宝利, 任顺祥, 孙同兴, 林莉, 邝灼彬, 2001. 广州地区烟粉虱寄主植物调查初报. 华南农业大学学报, 22: 43 - 47]

Qiu BL, Ren SX, Wen SY, Mandour SN, 2006. Population differentiation of three biotypes of *Bemisia tabaci* in China by DNA polymorphism. *J. South China Agric. Univ.*, 27: 29 - 34. [邱宝利, 任顺祥, 温硕洋, Mandour SN, 2006. 中国3种不同生物型烟粉虱的种群DNA多态性研究. 华南农业大学学报, 27: 29 - 34]

Reitz SR, 2007. Ecology: Invasion of the whiteflies. *Science*, 318: 1 733 - 1 734

Secker AE, Bedford IA, Markham PG, De Courcy-Williams ME, 1998. Squash, a reliable field indicator for the presence of B biotype of tobacco whitefly, *Bemisia tabaci*. In: Brighton Crop Protection Conference - Pest and Diseases. British Crop Protection Council. 837 - 842.

Shen Y, 2007. Studies on Biotypes of *Bemisia tabaci* (Homoptera: Aleyrodidae) in Several Areas of China. MSc Thesis, Yangzhou University, Yangzhou, Jiangsu. 28 - 32. [沈媛, 2007, 中国部分地区烟粉虱生物鉴定, 江苏扬州: 扬州大学硕士学位论文. 28 - 32]

Xu J, Wang WL, Liu SS, 2006. The occurrence and infestation of *Bemisia tabaci* biotype Q in partial regions of Zhejiang province. *Plant Protection*, 32: 121. [徐婧, 王文丽, 刘树生, 2006. Q型烟粉虱在浙江局部地区大量发生危害. 植物保护, 32: 121]

Zang LS, Liu SS, 2007. A comparative study on mating behavior between the B biotype and a non-B biotype of *Bemisia tabaci* (Hemiptera: Aleyrodidae) from Zhejiang, China. *J. Insect Behav.*, 20: 157 - 171.

Zhang LP, Zhang YJ, Zhang WJ, Wu QJ, Xu BY, Chu D, 2005. Analysis of genetic diversity among different geographical populations and determination of biotypes of *Bemisia tabaci* in China. *J. Appl. Entomol.*, 129: 121 - 128.

Zhou FC, Du YZ, Sun W, Yu GJ, Gong WR, Lu ZQ, Ren SX, 2004. Investigation of host plant of *Bemisia tabaci* and evaluation of its occurrence in Jiangsu province. *J. Yangzhou Univ.* (*Agricultural and Life Science Edition*), 24: 71 - 74. [周福才, 杜予州, 孙伟, 于淦军, 龚伟荣, 陆自强, 任顺祥, 2004. 江苏省烟粉虱寄主植物调查及其危害评价. 扬州大学学报(农业与生命科学版), 24: 71 - 74]

华东、华南和西南地区烟粉虱的种群及寄主分化

Muhammad Z. AHMED[1], 沈　媛[2], 金桂华[1], 任顺祥[1,*], 杜予州[2], 邱宝利[1]

(1. 华南农业大学资环学院昆虫学系, 广州 510640; 2. 扬州大学园艺与植物保护学院, 江苏扬州 225009)

摘要: 烟粉虱 *Bemisia tabaci* 是一个复合种,它具有的生物型分化、较强的传播病毒的能力和抗药性、较快的繁殖速率等特征使其成为我国农业生产中重要害虫之一。本研究利用细胞色素线粒体氧化酶Ⅰ基因,对采集自江苏、广东和云南三省的烟粉虱样本进行了生物型鉴定,并对烟粉虱生物型与寄主植物之间的关联性开展了调查。结果表明,在广东和云南省,都存在未鉴定的土著种群与入侵的B型、Q型共存的现象;同时,在本研究中广东省尚未采集到Q型烟粉虱,而在江苏采集到的粉虱样本全部为入侵型。研究结果还表明,相对于入侵种而言,土著种群显示出更强的寄主植物趋同性;丰富的寄主植物以及本身具有的多食性特性有助于B型、Q型等生物型在世界各地的广泛入侵。

关键词: 烟粉虱; 生物型; 寄主植物; 地理分布; 中国

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